

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2002, 19:53:16 : Search time 2690 Seconds  
(without alignments)  
16498.803 Million cell updates/sec

Title: US-10-025-514-7

Perfect score: 1525

Sequence: 1 tctagaccatgtctggaag.....ccaactcagaagttagtcgac 1525

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEnbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pi:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pi:\*

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27: em\_sts:\*

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29: em\_vi:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pln:\*

35: em\_htg\_rod:\*

36: em\_htg\_mam:\*

37: em\_htg\_vrt:\*

38: em\_sy:\*

39: em\_htgo\_hum:\*

40: em\_htgo\_mus:\*

41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	630.4	41.3	1308	6	AR111412
2	629.4	41.3	1185	6	AR111411
3	442.4	29.0	1345	6	AR111411
4	438	28.7	1434	6	HOMAIATB
5	436.4	28.6	1312	6	E00631
6	434.8	28.5	1584	9	BC011991
7	433.2	28.4	1352	6	AX335339
8	433.2	28.4	1352	6	HUMALATM
9	433.2	28.4	1371	6	AX335338
10	433.2	28.4	1371	9	HSATPR1
11	433.2	28.4	1399	9	AK026174
12	433.2	28.4	1434	6	E00195
13	433.2	28.4	1434	6	I04196
14	433.2	28.4	1434	6	I04272
15	433.2	28.4	1434	6	I07849
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# ALIGNMENTS

RESULT 1	AR111412	Sequence	6 from patent US 6127145.	DNA	linear	PAT 14-FEB-2001
LOCUS	AR111412	Sequence	1308 bp	DNA		
DEFINITION	AR111412	Sequence	6 from patent US 6127145.	DNA		
ACCESSION	AR111412	Sequence	1308 bp	DNA		
VERSION	AR111412.1	Sequence	1308 bp	DNA		
KEYWORDS	AR111412.1	Sequence	1308 bp	DNA		
SOURCE	Unknown.	Sequence	1308 bp	DNA		
ORGANISM	Unknown.	Sequence	1308 bp	DNA		
REFERENCE	1 (bases 1 to 1308)	Sequence	1308 bp	DNA		
AUTHORS	Sutliff, R.D. and Rodriguez, R.L.	Sequence	1308 bp	DNA		
TITLE	Production of .alpha..sub.1 -antitrypsin in plants	Sequence	1308 bp	DNA		
JOURNAL	Patent: US 6127145-A 6 03-OCT-2000;	Sequence	1308 bp	DNA		
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QY	1295	TGTTACTCAAGAGCTCCATTAAATTTAGTAAAGCTGTTTCACAAAGCCGCTCTTAACATAT	1354
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Db	1136	CGACGAGAGGAGGAGGAGCTGCGGGGCGCATGTTCTGAGAGCCATCCCATGTCCAT	1195
QY	1415	TCACACAGAAGTTAAATTTAATAACCATTCGTTTCTGATGATCGAGCAACACTAA	1474
Db	1196	CCGCGCCGAGGTCAAGTTCAACAAGCCCTTCGTTCTCTGATGATCGAGCAACAGAA	1255
QY	1475	AAGCCCATTTGTTATGGTAAAGTTGTCAACCCCAACTCAGAAGT	1518
Db	1256	GAGCCCTCTTCATGGGAGGTGCTCAACCCAGCAGAAGT	1299
RESULT 2			
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LOCUS	Sequence 3 from patent US 6127145.		
DEFINITION	AR111411		
ACCESSION	AR111411		
VERSION	AR111411.1	GI:12828259	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1185)		
AUTHORS	Sutliff, T.D. and Rodriguez, R.L.		
TITLE	Production of .alpha. sub.1 -antitrypsin in plants		
JOURNAL	Patent: US 6127145-A 3 03-OCT-2000;		
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	source		
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	Matches	837;	Conservative 0; Mismatches 346; Indels 0; Gaps 0;
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QY	396	CCGACTTTTAAATAAATTAATCTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACA	455
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QY	516	TTGCGCATTTGAGTTTATAGTTACTTAAAGCCGATACCATGACGAGATTTTAGAGGTTTA	575
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QY	636	AGAATCTTGAATCAACCTGATTTCTCAATTTGAATTAATACTACTGTAACGGTTTATTTTG	695
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QY	696	TCGTAAGGTTTAAATTTGGTTGCAAAATTCCTAGAGAGCTCAAGAACTATATCATAGT	755
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QY	756	GAGGCTTTTACGTTAATTTTGGTGATCTCAGGAAGCTAAAAAGCAAAATTAATGATTAT	815
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E00631
LOCUS E00631 1434 bp RNA linear PAT 29-SEP-1997
DEFINITION DNA encoding human alpha-1 antitrypsin mutain.
ACCESSION E00631
VERSION E00631.1 GI:2168910
KEYWORDS JP 1986012289-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1434)
AUTHORS Maagaretso,W.I. and Guren,H.K.
TITLE REGION SPECIFIC MUTATION INDUCTION IN ALPHA-1-ANTI-TRYPsin
JOURNAL Patent: JP 1986012289-A 1 20-JAN-1986;
CHIMO JIENETEITSUKUSU INC
COMMENT OS human
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PN JP 1986012289-A/1
PD 20-JAN-1986
PF 14-MAR-1984 US 84 589410, 07-MAR-1985 US 85 709382 PI
PR 14-MAR-1984 US 84 589410, 07-MAR-1985 US 85 709382 PI
MAAGARETSUTO WAI INZURIL, GUREN HITOSHI KAWASAKI PC
C12N15/00,A61K35/74,A61K37/64,C07H21/04,C07K15/04, PC
C12P21/02//A61K37/04,
PC C12N9/99,(C12P21/02,C12R1:865);
CC strandedness: Both;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue_type=livest;
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Matches 732; Conservative 0; Mismatches 490; Indels 0; Gaps 0;
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RESULT 5
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DEFINITION Sequence 1 from Patent US 4599311. linear PAT 21-MAY-1993
ACCESSION I02706
VERSION I02706.1 GI:268359
KEYWORDS
SOURCE Unknown.
ORGANISM Unclonified.
REFERENCE 1 (bases 1 to 1312)
AUTHORS Kawasaki G.H.
TITLE Glycolytic promoters for regulated protein expression: protease inhibitor
JOURNAL Patent: US 4599311-A 1 08-JUL-1986;
1547 - 16th Ave. East; Seattle, WA
FEATURES Location/Qualifiers
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source 1..1312
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Best Local Similarity 59.8%; Pred. No. 1.1e-83;
Matches 731; Conservative 0; Mismatches 491; Indels 0; Gaps 0;
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BC011991 1584 bp mRNA linear PRI 02-AUG-2001  
LOCUS Homo sapiens, Similar to serine (or cysteine) proteinase inhibitor,  
DEFINITION clade A (alpha-1 antiproteinase, antitrypsin), member 1, clone  
MGC:9222 IMAGE:3859644, mRNA, complete cds.  
ACCESSION BC011991  
VERSION BC011991.1 GI:15080498  
KEYWORDS MGC.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1584)  
Strausberg,R.  
Direct Submission  
Submitted (30-JUL-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue procurement: DCTD/DRP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [villalon@bcm.tmc.edu](mailto:villalon@bcm.tmc.edu)  
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,  
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,  
Muzny,D.M., Gibbs,R.A.  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 21 Row: d Column: 6  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 6855600.  
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Best Local Similarity 59.7%; Pred. No. 2.5e-83;  
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HUMALATM		1352 bp	mRNA	linear	PRI 01-NOV-1994
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DEFINITION					
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VERSION					
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RESULT 11
AK026174
LOCUS
DEFINITION
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AF113676 Homo sapiens clone FUB2803 PRO0684 mRNA.
ACCESSION
AK026174
VERSION
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KEYWORDS
oligo capping; fis (full insert sequence).
SOURCE
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (sites)
Kawabata,A., Hiki,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1399)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:cdna1@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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Best Local Similarity 59.7%   Pred. No. 5.5e-83;
Matches 729; Conservative 0; Mismatches 493; Indels 0; Gaps 0;

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Job time : 2703 secs

